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Malaria, dynamic epidemiology in flood affected area od District Muzafar Garh, Punjab, Pakistan in 2010

S. Hassan [1,*], M. Murtaza [2]

[1] *Medicine, Lahore, Punjab, Pakistan*
[2] *Medicine, Ali Pur, Pakistan*

Background: Pakistan had country's history worst floods in August 2010 and water surrounding populated areas added mosquito breeding sites hence, increased malariogenic potential. Pakistan in control phase of Malaria eradication efforts, in year 2009 reported 167579 confirmed Malaria cases. Muzafar Garh was one of the worst flood hit district where 1420 Malaria cases were reported by September in year 2010. We analysed Malaria surveillance data from a tehsil of District Muzafar Garh.

Methods: All the public sector hospitals of tehsil Ali Pur, having Malaria investigation facilities from Aug-Nov, 2010 have contributed data in this data review study. To know flood's effects on potential increase in malaria incidence, previous year's data for similar months is taken as baseline figures. Database was prepared in Microsoft Excel and data analysis was performed using Epiinfo software version 3.5.1®.

Results: Though after even after floods, Malaria endemicity is of low transmission level (<1 per 1000 persons), yet there is four times increased confirmed cases in year 2010 as compared to year 2009. From Aug to Nov Slide positive rate (SPR) increased from 18 to 26% compared to 18 to 16% a year prior and Falciparum positive cases rate climbed from 18% in 2009 to 34% in 2010. Majority of the patients (71%) are from rural areas, while most of them are male (61%) and are of 15-49 year age group.

Conclusion: Though overall endemicity is at low transmission level, yet there is rise in other indicators like SPR and Falciparum positive cases from previous baseline of 20% and 30% respectively. Disease burden may be even higher as private sector and people taking over the counter treatment are not part of above mentioned figures. Use of Rapid diagnostic tests, preventive strategies like mass drug administration as prophylaxis, and insecticide treated nets may help lessen the disease burden.

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The changing serological profile of hepatitis A in Victoria, Australia: a comparison of three time points

A. Heywood [1,*], A. Newall [1], Z. Gao [1], J. Wood [1], A. Breschkin [2], S. Nicholson [3], H. Gidding [4], D. Dwyer [5], L. Gilbert [6], P. McIntyre [7], R. MacIntyre [1]

[1] *University of New South Wales, Sydney, Australia*
[2] *Victorian Infectious Disease Research Laboratory, Melbourne, Australia*
[3] *Victorian Infectious Disease Research Laboratory, Melbourne, VIC, Australia*
[4] *University of New South Wales, Sydney, NSW, Australia*
[5] *Westmead Hospital, Sydney, Australia*
[6] *Institute for Clinical Pathology and Medical Research, Sydney, NSW, Australia*
[7] *National Centre for Immunisation Research asnd Surveillance, Sydney, NSW, Australia*

Background: Serological data provides an important measure of past exposure and immunity to hepatitis A virus (HAV) infection in a population. National serosurveys from developed counties have typically indicated a decline in HAV seroprevalence over time as sanitation levels improve. The potential for temporal and age-related changes in HAV susceptibility make it important to monitor the serological profile of a population.

Methods: We examined trends in the seroepidemiology of HAV in Victoria, Australia, drawing on cross-sectional samples taken at three time points over a 20 year period. Stored sera from 1988 (n = 753), 1998 (n = 1091), and 2008 (n = 791) from persons aged 1-69 years were obtained from the state of Victoria, Australia. HAV seropositivity estimates for each sample were standardised by age and gender to mid-year population estimates. Additional data were obtained on disease notification, population level migration and travel data and manufacturer vaccine sales data.

Results: The within-year population adjusted results show a significant trend of increasing population HAV seroprevalence over time from 34.3% (95% CI 31.7-36.9) in 1988, to 40.0% (95% CI 37.1-42.8) in 1998 and 55.1% (95% CI 52.1-58.1) in 2008, $P < 0.0001$. A particularly dramatic rise in population seroprevalence was observed between 1998 and 2008 in those aged 5-39 years. No significant change over time was observed for those aged 40-69 years. The increase in HAV seropositivity over time is in contrast to the declining rates of disease notification in Australia. Travel to endemic regions, migration to Australia from endemic regions and vaccine uptake have increased over the study period in Australia.

Conclusion: Based on comparisons with other Australian data, it appears the increase in population seroprevalence over the last two decades is unlikely to be due to endemic transmission of infection. Instead, other factors, including increases in travel to endemic regions, migration to Australia and vaccine uptake are more likely causes. Ongoing monitoring of HAV serological profiles is required to determine future policy direction to prevent increased burden.

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